

0590
1123

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OIPE

RAW SEQUENCE LISTING

DATE: 12/14/2001

PATENT APPLICATION: US/09/728,721

TIME: 16:03:41

Input Set : N:\Crf3\RULE60\09728721.txt

Output Set: N:\CRF3\12142001\I728721.raw

4 <110> APPLICANT: Bertin, John
 6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
 THEREOF

8 <130> FILE REFERENCE: 07334-124001
 10 <140> CURRENT APPLICATION NUMBER: 09/728,721
 11 <141> CURRENT FILING DATE: 2000-12-01
 13 <150> PRIOR APPLICATION NUMBER: 09/340,620
 14 <151> PRIOR FILING DATE: 1999-06-28
 16 <150> PRIOR APPLICATION NUMBER: US 09/207,359
 17 <151> PRIOR FILING DATE: 1998-12-08
 19 <150> PRIOR APPLICATION NUMBER: US 09/099,041
 20 <151> PRIOR FILING DATE: 1998-06-17
 22 <150> PRIOR APPLICATION NUMBER: US 09/019,942
 23 <151> PRIOR FILING DATE: 1998-02-06
 25 <160> NUMBER OF SEQ ID NOS: 71
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1931
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (214)...(1833)
 38 <400> SEQUENCE: 1

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40	tggggcgccct cgtgacctag tggtgcgggg caaaaagggt cttgccggcc tcgctcgtgc	120
41	agggggcgtat ctggggcgct gagcgcggcg tgggagcctt gggagccgcc gcagcagggg	180
42	gcacacccgg aaccggcctg agcgcgggg acc atg aac ggg gag gcc atc tgc	234
43	Met Asn Gly Glu Ala Ile Cys	
44	1 5	
46	agc gcc ctg ccc acc att ccc tac cac aaa ctc gcc gac ctg cgc tac	282
47	Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr	
48	10 15 20	
50	ctg agc cgc ggc gcc tct ggc act gtg tcg tcc gcc cgc cac gca gac	330
51	Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp	
52	25 30 35	
54	tgg cgc gtc cag gtg gcc gtg aag cac ctg cac atc cac act ccg ctg	378
55	Trp Arg Val Gln Val Ala Val Lys His Leu His Ile His Thr Pro Leu	
56	40 45 50 55	
58	ctc gac agt gaa aga aag gat gtc tta aga gaa gct gaa att tta cac	426
59	Leu Asp Ser Glu Arg Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His	
60	60 65 70	
62	aaa gct aga ttt agt tac att ctt cca att ttg gga att tgc aat gag	474
63	Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu	
64	75 80 85	
66	cct gaa ttt ttg gga ata gtt act gaa tac atg cca aat gga tca tta	522
67	Pro Glu Phe Leu Gly Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu	
68	90 95 100	

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70 aat gaa ctc cta cat agg aaa act gaa tat cct gat gtt gct tgg cca      570
71 Asn Glu Leu Leu His Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro
72      105                      110                      115
74 ttg aga ttt cgc atc ctg cat gaa att gcc ctt ggt gta aat tac ctg      618
75 Leu Arg Phe Arg Ile Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu
76 120                      125                      130                      135
78 cac aat atg act cct cct tta ctt cat cat gac ttg aag act cag aat      666
79 His Asn Met Thr Pro Pro Leu Leu His His Asp Leu Lys Thr Gln Asn
80      140                      145                      150
82 atc tta ttg gac aat gaa ttt cat gtt aag att gca gat ttt ggt tta      714
83 Ile Leu Leu Asp Asn Glu Phe His Val Lys Ile Ala Asp Phe Gly Leu
84      155                      160                      165
86 tca aag tgg cgc atg atg tcc ctc tca cag tca cga agt agc aaa tct      762
87 Ser Lys Trp Arg Met Met Ser Leu Ser Gln Ser Arg Ser Ser Lys Ser
88      170                      175                      180
90 gca cca gaa gga ggg aca att atc tat atg cca cct gaa aac tat gaa      810
91 Ala Pro Glu Gly Gly Thr Ile Ile Tyr Met Pro Pro Glu Asn Tyr Glu
92      185                      190                      195
94 cct gga caa aaa tca agg gcc agt atc aag cac gat ata tat agc tat      858
95 Pro Gly Gln Lys Ser Arg Ala Ser Ile Lys His Asp Ile Tyr Ser Tyr
96 200                      205                      210                      215
98 gca gtt atc aca tgg gaa gtg tta tcc aga aaa cag cct ttt gaa gat      906
99 Ala Val Ile Thr Trp Glu Val Leu Ser Arg Lys Gln Pro Phe Glu Asp
100      220                      225                      230
102 gtc acc aat cct ttg cag ata atg tat agt gtg tca caa gga cat cga      954
103 Val Thr Asn Pro Leu Gln Ile Met Tyr Ser Val Ser Gln Gly His Arg
104      235                      240                      245
106 cct gtt att aat gaa gaa agt ttg cca tat gat ata cct cac cga gca      1002
107 Pro Val Ile Asn Glu Glu Ser Leu Pro Tyr Asp Ile Pro His Arg Ala
108      250                      255                      260
110 cgt atg atc tct cta ata gaa agt gga tgg gca caa aat cca gat gaa      1050
111 Arg Met Ile Ser Leu Ile Glu Ser Gly Trp Ala Gln Asn Pro Asp Glu
112      265                      270                      275
114 aga cca tct ttc tta aaa tgt tta ata gaa ctt gaa cca gtt ttg aga      1098
115 Arg Pro Ser Phe Leu Lys Cys Leu Ile Glu Leu Glu Pro Val Leu Arg
116 280                      285                      290                      295
118 aca ttt gaa gag ata act ttt ctt gaa gct gtt att cag cta aag aaa      1146
119 Thr Phe Glu Glu Ile Thr Phe Leu Glu Ala Val Ile Gln Leu Lys Lys
120      300                      305                      310
122 aca aag tta cag agt gtt tca agt gcc att cac cta tgt gac aag aag      1194
123 Thr Lys Leu Gln Ser Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys
124      315                      320                      325
126 aaa atg gaa tta tct ctg aac ata cct gta aat cat ggt cca caa gag      1242
127 Lys Met Glu Leu Ser Leu Asn Ile Pro Val Asn His Gly Pro Gln Glu
128      330                      335                      340
130 gaa tca tgt gga tcc tct cag ctc cat gaa aat agt ggt tct cct gaa      1290
131 Glu Ser Cys Gly Ser Ser Gln Leu His Glu Asn Ser Gly Ser Pro Glu
132      345                      350                      355
134 act tca agg tcc ctg cca gct cct caa gac aat gat ttt tta tct aga      1338

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135 Thr Ser Arg Ser Leu Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg
136 360 365 370 375
138 aaa gct caa gac tgt tat ttt atg aag ctg cat cac tgt cct gga aat 1386
139 Lys Ala Gln Asp Cys Tyr Phe Met Lys Leu His His Cys Pro Gly Asn
140 380 385 390
142 cac agt tgg gat agc acc att tct gga tct caa agg gct gca ttc tgt 1434
143 His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys
144 395 400 405
146 gat cac aag acc att cca tgc tct tca gca ata ata aat cca ctc tca 1482
147 Asp His Lys Thr Ile Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser
148 410 415 420
150 act gca gga aac tca gaa cgt ctg cag cct ggt ata gcc cag cag tgg 1530
151 Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp
152 425 430 435
154 atc cag agc aaa agg gaa gac att gtg aac caa atg aca gaa gcc tgc 1578
155 Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys
156 440 445 450 455
158 ctt aac cag tcg cta gat gcc ctt ctg tcc agg gac ttg atc atg aaa 1626
159 Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys
160 460 465 470
162 gag gac tat gaa ctt gtt agt acc aag cct aca agg acc tca aaa gtc 1674
163 Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val
164 475 480 485
166 aga caa tta cta gac act act gac atc caa gga gaa gaa ttt gcc aaa 1722
167 Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys
168 490 495 500
170 gtt ata gta caa aaa ttg aaa gat aac aaa caa atg ggt ctt cag cct 1770
171 Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro
172 505 510 515
174 tac ccg gaa ata ctt gtg gtt tct aga tca cca tct tta aat tta ctt 1818
175 Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu
176 520 525 530 535
178 caa aat aaa agc atg taagtgactg tttttcaaga agaaatgtgt ttcataaaag 1873
179 Gln Asn Lys Ser Met
180 540
182 gatatttata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1931
184 <210> SEQ ID NO: 2
185 <211> LENGTH: 540
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 2
190 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
191 1 5 10 15
192 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
193 20 25 30
194 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
195 35 40 45
196 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
197 50 55 60

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198 Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro
199 65 70 75 80
200 Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
201 85 90 95
202 Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
203 100 105 110
204 Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
205 115 120 125
206 Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His
207 130 135 140
208 His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
209 145 150 155 160
210 Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
211 165 170 175
212 Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
213 180 185 190
214 Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
215 195 200 205
216 Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
217 210 215 220
218 Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
219 225 230 235 240
220 Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
221 245 250 255
222 Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
223 260 265 270
224 Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile
225 275 280 285
226 Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
227 290 295 300
228 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
229 305 310 315 320
230 Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
231 325 330 335
232 Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
233 340 345 350
234 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
235 355 360 365
236 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
237 370 375 380
238 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
239 385 390 395 400
240 Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Ile Pro Cys Ser Ser
241 405 410 415
242 Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
243 420 425 430
244 Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
245 435 440 445
246 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu

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Input Set : N:\Crif3\RULE60\09728721.txt

Output Set: N:\CRF3\12142001\I728721.raw

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247      450      455      460
248 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
249 465      470      475      480
250 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
251      485      490      495
252 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
253      500      505      510
254 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
255      515      520      525
256 Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
257      530      535      540
259 <210> SEQ ID NO: 3
260 <211> LENGTH: 1620
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 3
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266 ctgcgtacc tgagccgcgg cgcctctggc actgtgtcgt ccgcccgcga cgcagactgg      120
267 cgcgtccagg tggccgtgaa gcacctgcac atccacactc cgctgctcga cagtgaaga      180
268 aaggatgtct taagagaagc tgaaatttta cacaagcta gatttagtta cattcttcca      240
269 attttgggaa tttgcaatga gcctgaattt ttgggaatag ttactgaata catgccaaat      300
270 ggatcattaa atgaactcct acataggaaa actgaatata ctgatgttgc ttggccattg      360
271 agatttcgca tcctgcatga aattgccctt ggtgtaaatt acctgcacaa tatgactcct      420
272 cctttaacttc atcatgactt gaagactcag aatatcttat tggacaatga atttcatgtt      480
273 aagattgcag attttggttt atcaaagtgg cgcattgatgt ccctctcaca gtcacgaagt      540
274 agcaaatctg caccagaagg agggacaatt atctatatgc cacctgaaaa ctatgaacct      600
275 ggacaaaaat caagggccag tatcaagcac gatatatata gctatgcagt tatcacatgg      660
276 gaagtgttat ccagaaaaca gccttttgaa gatgtcacca atcctttgca gataatgtat      720
277 agtgtgtcac aaggacatcg acctgttatt aatgaagaaa gtttgccata tgatatacct      780
278 caccgagcac gtatgatctc tctaatagaa agtggatggg cacaaaatcc agatgaaaga      840
279 ccattcttct taaaatgttt aatagaactt gaaccagttt tgagaacatt tgaagagata      900
280 acttttcttg aagctgttat tcagctaaaag aaaacaaagt tacagagtgt ttcaagtgcc      960
281 attcacctat gtgacaagaa gaaaatggaa ttatctctga acatacctgt aaatcatggt      1020
282 ccacaagagg aatcatgtgg atcctctcag ctccatgaaa atagtggttc tcctgaaact      1080
283 tcaaggtccc tgccagctcc tcaagacaat gattttttat ctagaaaagc tcaagactgt      1140
284 tattttatga agctgcatca ctgtcctgga aatcacagtt gggatagcac catttctgga      1200
285 tctcaaaggg ctgattctg tgatcacaag accattccat gctcttcagc aataataaat      1260
286 ccactctcaa ctgcaggaaa ctcagaacgt ctgcagcctg gtatagccca gcagtggatc      1320
287 cagagcaaaa gggaagacat tgtgaaccaa atgacagaag cctgccttaa ccagtcgcta      1380
288 gatgcccttc tgtccaggga cttgatcatg aaagaggact atgaacttgt tagtaccaag      1440
289 cctacaagga cctcaaaagt cagacaatta ctagacacta ctgacatcca aggagaagaa      1500
290 tttgccaaag ttatagtaca aaaattgaaa gataacaaac aaatgggtct tcagccttac      1560
291 ccggaaatac ttgtggtttc tagatcacca tctttaaatt tacttcaaaa taaaagcatg      1620
293 <210> SEQ ID NO: 4
294 <211> LENGTH: 300
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 4
299 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/728,721

DATE: 12/14/2001

TIME: 16:03:42

Input Set : N:\Crf3\RULE60\09728721.txt

Output Set: N:\CRF3\12142001\I728721.raw

L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:4045 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:4057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71